



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

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Atty. Docket No: 1478-R-00

In re patent application of

LAZDUNSKI, MICHEL et al.

Serial No. 09/975,456

Filed: October 11, 2001

For: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2

STATEMENT TO SUPPORT FILING AND SUBMISSION IN
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

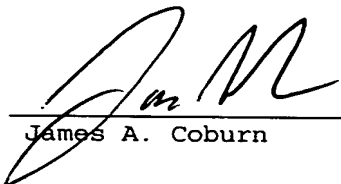
1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;
2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and
3. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United

Serial No. 09/975,456

States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

Nov. 9, 2001
Date


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SEQUENCE LISTING

<110> LAZDUNSKI, MICHEL
LAMBEAU, GERARD
VALENTIN, EMMANUEL

<120> NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2

<130> 1478-R-00

<140> 09/975,456

<141> 2001-10-11

<150> 60/239,491

<151> 2000-10-11

<160> 10

<170> PatentIn version 2.1

<210> 1

<211> 507

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(507)

<223> cDNA encoding human group IIF secreted phospholipase A2

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| 1 5 10 15 | |

| | |
|---|----|
| aca gct cac ggc agc ctg ctc aac ctg aag gcc atg gtg gag gcc gtc | 96 |
| Thr Ala His Gly Ser Leu Leu Asn Leu Lys Ala Met Val Glu Ala Val | |
| 20 25 30 | |

| | |
|---|-----|
| aca ggg agg agc gcc atc ctg tcc ttc gtg ggc tac ggt tgc tac tgt | 144 |
| Thr Gly Arg Ser Ala Ile Leu Ser Phe Val Gly Tyr Gly Cys Tyr Cys | |
| 35 40 45 | |

| | |
|---|-----|
| ggg ctg ggg ggc cgt ggc cag ccc aag gat gag gtg gac tgg tgc tgc | 192 |
| Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Glu Val Asp Trp Cys Cys | |
| 50 55 60 | |

| | |
|---|-----|
| cac gcc cac gac tgc tgc tac cag gaa ctc ttt gac caa ggc tgt cac | 240 |
| His Ala His Asp Cys Cys Tyr Gln Glu Leu Phe Asp Gln Gly Cys His | |
| 65 70 75 80 | |

| | |
|---|-----|
| ccc tat gtg gac cac tat gat cac acc atc gag aac aac act gag ata | 288 |
| Pro Tyr Val Asp His Tyr Asp His Thr Ile Glu Asn Asn Thr Glu Ile | |
| 85 90 95 | |

| | |
|---|-----|
| gtc tgc agt gac ctc aac aag aca gag tgt gac aag cag aca tgc atg | 336 |
| Val Cys Ser Asp Leu Asn Lys Thr Glu Cys Asp Lys Gln Thr Cys Met | |
| 100 105 110 | |

tgt gac aag aac atg gtt ctg tgc ctc atg aac cag acg tac cga gag 384
 Cys Asp Lys Asn Met Val Leu Cys Leu Met Asn Gln Thr Tyr Arg Glu
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gag tac cgt ggc ttc ctc aat gtc tac tgc cag ggc ccc acg ccc aac 432
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 130 135 140

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 35 40 45
 Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Glu Val Asp Trp Cys Cys
 50 55 60
 His Ala His Asp Cys Cys Tyr Gln Glu Leu Phe Asp Gln Gly Cys His
 65 70 75 80
 Pro Tyr Val Asp His Tyr Asp His Thr Ile Glu Asn Asn Thr Glu Ile
 85 90 95
 Val Cys Ser Asp Leu Asn Lys Thr Glu Cys Asp Lys Gln Thr Cys Met
 100 105 110
 Cys Asp Lys Asn Met Val Leu Cys Leu Met Asn Gln Thr Tyr Arg Glu
 115 120 125
 Glu Tyr Arg Gly Phe Leu Asn Val Tyr Cys Gln Gly Pro Thr Pro Asn
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 Cys Ser Ile Tyr Glu Pro Pro Pro Glu Glu Val Thr Cys Ser His Gln
 145 150 155 160
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 35 40 45
 Cys Tyr Cys Gly Leu Gly Gly Ser Gly Thr Pro Val Asp Glu Leu Asp
 50 55 60
 Lys Cys Cys Gln Thr His Asp Asn Cys Tyr Asp Gln Ala Lys Lys Leu
 65 70 75 80
 Asp Ser Cys Lys Phe Leu Leu Asp Asn Pro Tyr Thr His Thr Tyr Ser
 85 90 95
 Tyr Ser Cys Ser Gly Ser Ala Ile Thr Cys Ser Ser Lys Asn Lys Glu
 100 105 110
 Cys Glu Ala Phe Ile Cys Asn Cys Asp Arg Asn Ala Ala Ile Cys Phe
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Tyr Cys Gln Ser
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Thr Gly Lys Glu Ala Ala Leu Ser Tyr Gly Phe Tyr Gly Cys His Cys
35 40 45
Gly Val Gly Gly Arg Gly Ser Pro Lys Asp Ala Thr Asp Arg Cys Cys
50 55 60
Val Thr His Asp Cys Cys Tyr Lys Arg Leu Glu Lys Arg Gly Cys Gly
65 70 75 80
Thr Lys Phe Leu Ser Tyr Lys Phe Ser Asn Ser Gly Ser Arg Ile Thr
85 90 95
Cys Ala Lys Gln Asp Ser Cys Arg Ser Gln Leu Cys Glu Cys Asp Lys
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Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly Cys His Cys
35 40 45
Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr Asp Trp Cys Cys
50 55 60
Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys Thr Gln Gly Cys Ser
65 70 75 80

Ile Tyr Lys Asp Tyr Tyr Arg Tyr Asn Phe Ser Gln Gly Asn Ile His
85 90 95

Cys Ser Asp Lys Gly Ser Trp Cys Glu Gln Gln Leu Cys Ala Cys Asp
100 105 110

Lys Glu Val Ala Phe Cys Leu Lys Arg Asn Leu Asp Thr Tyr Gln Lys
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Arg Leu Arg Phe Tyr Trp Arg Pro His Cys Arg Gly Gln Thr Pro Gly
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Cys
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35 40 45

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Trp Pro Val Asp Gln Thr Asp Trp Cys Cys His Ala His Asp Cys Cys
65 70 75 80

Tyr Gly Arg Leu Glu Lys Leu Gly Cys Glu Pro Lys Leu Glu Lys Tyr
85 90 95

Leu Phe Ser Val Ser Glu Arg Gly Ile Phe Cys Ala Gly Arg Thr Thr
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Cys Gln Arg Leu Thr Cys Glu Cys Asp Lys Arg Ala Ala Leu Cys Phe
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Lys Leu Cys Thr Gly Pro Thr Pro Pro Cys
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 20 25 30

Thr Gly Lys Asn Ala Leu Thr Asn Tyr Gly Phe Tyr Gly Cys Tyr Cys
 35 40 45

Gly Trp Gly Gly Arg Gly Thr Pro Lys Asp Gly Thr Asp Trp Cys Cys
 50 55 60

Trp Ala His Asp His Cys Tyr Gly Arg Leu Glu Lys Gly Cys Asn
 65 70 75 80

Ile Arg Thr Gln Ser Tyr Lys Tyr Arg Phe Ala Trp Gly Val Val Thr
 85 90 95

Cys Glu Pro Gly Pro Phe Cys His Val Asn Leu Cys Ala Cys Asp Arg
 100 105 110

Lys Leu Val Tyr Cys Leu Lys Arg Asn Leu Arg Ser Tyr Asn Pro Gln
 115 120 125

Tyr Gln Tyr Phe Pro Asn Ile Leu Cys Ser
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<212> PRT

<213> Homo sapiens

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 20 25 30

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 35 40 45

Pro Ile Ala Tyr Met Lys Tyr Gly Cys Phe Cys Gly Leu Gly Gly His
 50 55 60

Gly Gln Pro Arg Asp Ala Ile Asp Trp Cys Cys His Gly His Asp Cys
 65 70 75 80

Cys Tyr Thr Arg Ala Glu Glu Ala Gly Cys Ser Pro Lys Thr Glu Arg
 85 90 95

Tyr Ser Trp Gln Cys Val Asn Gln Ser Val Leu Cys Gly Pro Ala Glu
 100 105 110

Asn Lys Cys Gln Glu Leu Leu Cys Lys Cys Asp Gln Glu Ile Ala Asn
115 120 125

Cys Leu Ala Gln Thr Glu Tyr Asn Leu Lys Tyr Leu Phe Tyr Pro Gln
130 135 140

Phe Leu Cys Glu Pro Asp Ser Pro Lys Cys Asp
145 150 155